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SEQUENCE LISTING

<110> UNIVERSITY COLLEGE LONDON

<120> SCREEN METHOD

<130> N757518

<140> PCT/GB00/00226

<141> 2000-01-26

<150> GB 9901705.5

<151> 1999-01-26

<150> GB 9913066.8

<151> 1999-06-04

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<170> PatentIn Ver. 2.1

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Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser  
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gcc aag ggc gag gag gtg gac gtc gcc cgc gcg gaa cgg cag cac cag 144  
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gcc gtg gtg tgc gag gag acg gcc ctc atc acc cga ccc ggg gcg ccg 288  
Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro  
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agc cgg agg aag gag gtt gac atg atg aaa gaa gca tta gaa aaa ctt 336  
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 100 105 110

cag ctc aat ata gta gag atg aaa gat gaa aat gca act tta gat ggc 384  
 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly  
 115 120 125

gga gat gtt tta ttc aca ggc aga gaa ttt ttt gtg ggc ctt tcc aaa 432  
 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys  
 130 135 140

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 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp  
 145 150 155 160

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ttc tgc agc atg gct ggg cct aac ctg atc gca att ggg tct agt gaa 576  
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tct gca cag aag gcc ctt aag atc atg caa cag atg agt gac cac cgc 624  
 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg  
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 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr  
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gag tat cca gaa agt gca aag gtt tat gag aaa ctg aag gac cat atg 768  
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Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu  
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Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val  
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Ala Val-Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro  
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Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu  
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Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly  
115 120 125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys  
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180 185 190

Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg  
195 200 205

Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr  
210 215 220

Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu  
225 230 235 240

Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met  
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 Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro  
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 Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg  
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 Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp  
 115 120 125  
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 130 135 140  
 aat cac cga gga gct gag atc gtg gcg gac acg ttc cgg gac ttc gcc 480  
 Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala  
 145 150 155 160  
 gtc tcc act gtg cca gtc tcg ggt ccc tcc cac ctg cgc ggt ctc tgc 528  
 Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys  
 165 170 175  
 ggc atg ggg gga cct cgc act gtt gtg gca ggc agc agc gac gct gcc 576

Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala	
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caa aag gct gtc cgg gca atg gca gtg ctg aca gat cac cca tat gcc	624
Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala	
195 200 205	
tcc ctg acc ctc cca gat gac gca gct gct gac tgt ctc ttt ctt cgt	672
Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg	
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Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly	
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gat ctg ccc aac agc cag gag gca ctg cag aag ctc tct gat gtc acc	768
Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr	
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Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu	
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Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg  
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Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu  
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Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr  
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Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala  
 145 150 155 160

Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys  
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Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala  
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Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg  
 210 215 220

Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly  
 225 230 235 240

Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr  
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 Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu  
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Phe Val Glu Asp Ala Val Val Phe Arg Asn Val Ala Leu Ile Thr			
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Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu			
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gcc gtg gcc cgg ctc ggc tgc tcg gtg aac tgg gtg tgg gag ccg ggc	336		
Ala Val Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Glu Pro Gly			
100 105 110			
acc ctg gac ggc ggc gac gtc ctg aag atc ggc gac acg atc tac gtg	384		
Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val			
115 120 125			
gga cgc ggc ggc cgg acc aac gcg gcc ggt gtc cag cag ttg cgg gcg	432		
Gly Arg Gly Gly Arg Thr Asn Ala Ala Gly Val Gln Gln Leu Arg Ala			
130 135 140			
gcg ttc gag ccg ctg ggc gcc cgg gtc gtc gcc gtg ccc gtg agc aag	480		
Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys			
145 150 155 160			
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Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val			
165 170 175			
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Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe			
180 185 190			
ctg ccg gtg ccg gag gag tcg ggg gcg cac gtg gtg ctg ctc ggc ggg	624		
Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly			
195 200 205			
agc agg ctg ctg atg gcg gcg agc gcg ccc aag acg gcg gag ctg ctc	672		
Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu			
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Ala Asp Leu Gly His Glu Pro Val Leu Val Asp Ile Gly Glu Phe Glu			
225 230 235 240			
aag ctg gag ggc tgt gtg acg tgc ctc tcg gtc agg ctg cgc gag ctg	768		
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Tyr Asp

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Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val  
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Phe Val Glu Asp Ala Val Val Val Phe Arg Asn Val Ala Leu Ile Thr  
65 70 75 80

Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu  
85 90 95

Ala Val Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Glu Pro Gly  
100 105 110

Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val  
115 120 125

Gly Arg Gly Gly Arg Thr Asn Ala Ala Gly Val Gln Gln Leu Arg Ala  
130 135 140

Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys  
145 150 155 160

Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val  
165 170 175

Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe  
180 185 190

Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly  
195 200 205

Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu  
210 215 220

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Lys Leu Glu Gly Cys Val Thr Cys Leu Ser Val Arg Leu Arg Glu Leu



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Gly Leu Thr Ser Ser His Leu Gly Lys Pro Asp Tyr Ala Lys Ala Leu
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Glu Gln His Asn Ala Tyr Ile Arg Ala Leu Gln Thr Cys Asp Val Asp
  35          40          45

atc acc ctg ctg ccg ccg gac gaa cgc ttc ccc gac tcg gtg ttc gtc 192
Ile Thr Leu Leu Pro Pro Asp Glu Arg Phe Pro Asp Ser Val Phe Val
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Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val
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Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr
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gtg gaa gcc ggc gac atc atg atg gtc ggc gac cac ttc tac atc ggc 384
Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly
  115         120         125

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Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile
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Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val
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180 185 190

atc gag atc ccc gaa gag gag tcc tac gcc gcc aac tgc atc tgg gtc 624  
Ile Glu Ile Pro Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val  
195 200 205

aac gaa agg gtg atc atg ccc gcc ggc tat ccc cgg acc cgc gag aag 672  
Asn Glu Arg Val Ile Met Pro Ala Gly Tyr Pro Arg Thr Arg Glu Lys  
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atc gcc cgc ctc ggc tac cgg gtg atc gag gtg gac acc tcc gaa tat 720  
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Glu Asp Pro Val Leu Cys Thr Ser Arg Cys Ala Ile Ile Thr Arg Pro  
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Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val  
85 90 95

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100 105 110

Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly  
115 120 125

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 Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val  
 145 150 155 160  
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 Ala Ala Gly Glu Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile  
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 65 70 75 80

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145 150 155 160	
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195 200 205	
atc tgg tac ggc gac ccg gac aag gac cac ggc tcc tgc acc ctg gaa Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu	672
210 215 220	
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225 230 235 240	
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275 280 285	
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290 295 300	

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 305 310 315 320

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 Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys  
 325 330 335

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 Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg  
 340 345 350

gag caa tgg gac gac ggt aac aac gtg gtc tgc ctg gag ccg ggc gtg 1104  
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gtg gtc ggc tac gac cgc aac acc tac acc aac acc ctg ctg cgc aag 1152  
 Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys  
 370 375 380

gcc ggc gtc gag gtc atc acc atc agc gcc agc gaa ctg ggt cgc ggt 1200  
 Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly  
 385 390 395 400

cgc ggc ggc ggc cac tgc atg acc tgc ccg atc gtc cgc gac ccg atc 1248  
 Arg Gly Gly Gly His Cys Met Thr Cys Pro Ile Val Arg Asp Pro Ile  
 405 410 415

gac tac tga 1257  
 Asp Tyr

<210> 10  
 <211> 418  
 <212> PRT  
 <213> P. aeruginosa

<400> 10  
 Met Ser Thr Glu Lys Thr Lys Leu Gly Val His Ser Glu Ala Gly Lys  
 1 5 10 15

Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu  
 20 25 30

Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val  
 35 40 45

Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu  
 50 55 60

Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile  
 65 70 75 80

Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala  
 85 90 95

Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu  
 100 105 110  
 Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Gly Val Ala  
 115 120 125  
 Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr  
 130 135 140  
 Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn  
 145 150 155 160  
 Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr  
 165 170 175  
 Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr  
 180 185 190  
 Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu  
 195 200 205  
 Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu  
 210 215 220  
 Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met  
 225 230 235 240  
 Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu  
 245 250 255  
 Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys  
 260 265 270  
 Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg  
 275 280 285  
 Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe  
 290 295 300  
 Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg  
 305 310 315 320  
 Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys  
 325 330 335  
 Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg  
 340 345 350  
 Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val  
 355 360 365  
 Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys  
 370 375 380  
 Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly

385                      390                      395                      400  
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                          405                                      410                                      415

Asp Tyr

<210> 11  
 <211> 1014  
 <212> DNA  
 <213> M. tuberculosis

<220>  
 <221> CDS  
 <222> (69)..(986)

<400> 11  
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gttggttt atg acg gat tcc tac gtc gct gct gcc cgt cta ggg tca cct 110  
           Met Thr Asp Ser Tyr Val Ala Ala Ala Arg Leu Gly Ser Pro  
           1                      5                                      10

gca cgc cgc acc ccc cgg acg cgg cgg tat gca atg acc ccg ccg gcc 158  
 Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala Met Thr Pro Pro Ala  
   15                      20                                      25                                      30

ttc ttt gcc gtc gca tac gcg atc aac ccc tgg atg gac gtc acc gcg 206  
 Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp Met Asp Val Thr Ala  
                          35                                      40                                      45

cca gtc gac gtc caa gtc gcg caa gca cag tgg gag cac ctc cac cag 254  
 Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp Glu His Leu His Gln  
                          50                                      55                                      60

acc tat ctt cgg cta ggc cac agc gtg gat ctg atc gag ccc att tcc 302  
 Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu Ile Glu Pro Ile Ser  
                          65                                      70                                      75

ggg tta ccg gac atg gtg tac acc gcc aac ggt ggg ttc atc gcg cac 350  
 Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly Gly Phe Ile Ala His  
   80                                      85                                      90

gac atc gcc gtg gtc gcc cgg ttc cgg ttc ccc gaa cga gct ggt gag 398  
 Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro Glu Arg Ala Gly Glu  
   95                      100                                      105                                      110

tct aga gcc tat gcc agc tgg atg tcc tcg gtc gga tat cgc ccg gtg 446  
 Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val Gly Tyr Arg Pro Val  
                          115                                      120                                      125

acc acc cgc cac gtc aac gag gga cag gcc gac ctg ctg atg gtt gcc 494  
 Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp Leu Leu Met Val Gly

130	135	140	
gaa agg gtg ttg gcg ggc tac ggc ttt cgc aca gac cag cgc gca cac	542		
Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr Asp Gln Arg Ala His			
145	150	155	
gcc gaa atc gcc gcg gtg ctt ggt ctg ccg gtg gtc tcc ctc gag ttg	590		
Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val Val Ser Leu Glu Leu			
160	165	170	
gtc gac cca cgg ttc tat cac ctg gac acc gcg ctg gcc gtg ctc gac	638		
Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala Leu Ala Val Leu Asp			
175	180	185	190
gac cac acg atc gcc tac tac ccg ccg gcg ttc agt acg gca gcg cag	686		
Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe Ser Thr Ala Ala Gln			
195	200	205	
gaa cag ttg tcg gcg ctg ttc ccc gac gcg att gtg gtc ggc agt gcc	734		
Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile Val Val Gly Ser Ala			
210	215	220	
gac gcg ttc gtg ttc gga ctc aac gcc gtc tct gac ggt ctg aac gta	782		
Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser Asp Gly Leu Asn Val			
225	230	235	
gtg ctt ccg gtc gcg gcc atg ggt ttt gcg gcg cag tta cgc gca gcc	830		
Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala Gln Leu Arg Ala Ala			
240	245	250	
ggc ttc gag ccg gtc ggt gtc gat ctg tcc gag ctg ctc aag ggc ggc	878		
Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu Leu Leu Lys Gly Gly			
255	260	265	270
ggt tcc gtc aag tgc tgc acg ctg gag ata cac cca tga caa atc tcg	926		
Gly Ser Val Lys Cys Cys Thr Leu Glu Ile His Pro Gln Ile Ser			
275	280	285	
cgg atg cca ctc agg cca cta tgg cac tgg tcg aaa ggc atg cag cgc	974		
Arg Met Pro Leu Arg Pro Leu Trp His Trp Ser Lys Gly Met Gln Arg			
290	295	300	
aca att att cgc cgctgcctgt ggtggcggcc agcgccta	1014		
Thr Ile Ile Arg			
305			

<210> 12

<211> 282

<212> PRT

<213> M. tuberculosis

<400> 12

Met	Thr	Asp	Ser	Tyr	Val	Ala	Ala	Ala	Arg	Leu	Gly	Ser	Pro	Ala	Arg
1					5					10				15	



Arg Thr Pro Arg Thr Arg Arg Tyr Ala Met Thr Pro Pro Ala Phe Phe  
20 25 30

Ala Val Ala Tyr Ala Ile Asn Pro Trp Met Asp Val Thr Ala Pro Val  
35 40 45

Asp Val Gln Val Ala Gln Ala Gln Trp Glu His Leu His Gln Thr Tyr  
50 55 60

Leu Arg Leu Gly His Ser Val Asp Leu Ile Glu Pro Ile Ser Gly Leu  
65 70 75 80

Pro Asp Met Val Tyr Thr Ala Asn Gly Gly Phe Ile Ala His Asp Ile  
85 90 95

Ala Val Val Ala Arg Phe Arg Phe Pro Glu Arg Ala Gly Glu Ser Arg  
100 105 110

Ala Tyr Ala Ser Trp Met Ser Ser Val Gly Tyr Arg Pro Val Thr Thr  
115 120 125

Arg His Val Asn Glu Gly Gln Gly Asp Leu Leu Met Val Gly Glu Arg  
130 135 140

Val Leu Ala Gly Tyr Gly Phe Arg Thr Asp Gln Arg Ala His Ala Glu  
145 150 155 160

Ile Ala Ala Val Leu Gly Leu Pro Val Val Ser Leu Glu Leu Val Asp  
165 170 175

Pro Arg Phe Tyr His Leu Asp Thr Ala Leu Ala Val Leu Asp Asp His  
180 185 190

Thr Ile Ala Tyr Tyr Pro Pro Ala Phe Ser Thr Ala Ala Gln Glu Gln  
195 200 205

Leu Ser Ala Leu Phe Pro Asp Ala Ile Val Val Gly Ser Ala Asp Ala  
210 215 220

Phe Val Phe Gly Leu Asn Ala Val Ser Asp Gly Leu Asn Val Val Leu  
225 230 235 240

Pro Val Ala Ala Met Gly Phe Ala Ala Gln Leu Arg Ala Ala Gly Phe  
245 250 255

Glu Pro Val Gly Val Asp Leu Ser Glu Leu Leu Lys Gly Gly Gly Ser  
260 265 270

Val Lys Cys Cys Thr Leu Glu Ile His Pro  
275 280

<210> 13  
<211> 305  
<212> PRT

<213> M. tuberculosis

<400> 13

Asn Val Ser Met Glu Asn Thr Gln Arg Pro Ser Phe Asp Cys Glu Ile  
1 5 10 15

Arg Ala Lys Tyr Arg Trp Phe Met Thr Asp Ser Tyr Val Ala Ala Ala  
20 25 30

Arg Leu Gly Ser Pro Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala  
35 40 45

Met Thr Pro Pro Ala Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp  
50 55 60

Met Asp-Val Thr Ala Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp  
65 70 75 80

Glu His Leu His Gln Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu  
85 90 95

Ile Glu Pro Ile Ser Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly  
100 105 110

Gly Phe Ile Ala His Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro  
115 120 125

Glu Arg Ala Gly Glu Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val  
130 135 140

Gly Tyr Arg Pro Val Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp  
145 150 155 160

Leu Leu Met Val Gly Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr  
165 170 175

Asp Gln Arg Ala His Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val  
180 185 190

Val Ser Leu Glu Leu Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala  
195 200 205

Leu Ala Val Leu Asp Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe  
210 215 220

Ser Thr Ala Ala Gln Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile  
225 230 235 240

Val Val Gly Ser Ala Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser  
245 250 255

Asp Gly Leu Asn Val Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala  
260 265 270

Gln Leu Arg Ala Ala Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu

275		280		285											
Leu	Leu	Lys	Gly	Gly	Gly	Ser	Val	Lys	Cys	Cys	Thr	Leu	Glu	Ile	His
290						295						300			

Pro  
305

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: UNIVERSITY COLLEGE LONDON  
(B) STREET: Gower Street  
(C) CITY: London  
(E) COUNTRY: United Kingdom  
(F) POSTAL CODE (ZIP): WC1E 6BT

(ii) TITLE OF INVENTION: SCREEN METHOD

(iii) NUMBER OF SEQUENCES: 12

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 858 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGGCCGGCC TGGCCACCC CTCGCTTC GCGCGGCCA CCCACCCGT GGTGCGGCG	60
CTACCCGAGT CGCTCTGCC GCACGCGTG AGAAGCGCA AGGCGAGGA GGTGACGTC	120
GCCCGCGCG AACCGCAGCA CAGCTCTAC GTGGCGGTGC TGGGCAGCA GCTGGGCTG	180
CAGTGCTGG AGTGCCGGC CGACGAGAG CTTCCGACT GCGTCTTGT GGAGACGTG	240
GCGTGCTGT GCGAGGAGC GGCCTCATC ACCCGACCG GGGCGCGAG CCGGAGGAAG	300
GAGTTGACA TGATGAAAG AGCATTAGAA AAATTCAGC TCAATATAG AGAGATGAAA	360
GATGAAATG CACTTTAGA TGGCGGAGT GTTTATTCA CAGGCAGAG ATTTTGTG	420
GGCCTTCCA AAAGBACAA TCAACAGGT GCTGAAATCT TGGCTGATC TTTTAAGGAC	480

TATGCAGTCT CCACAGTCCC AGTGSCAGAT GGGTTGCATT TGAAGAGTTT CTGCAGCATG 540  
 GCTGGGCCTA ACCTGATCGC AATTGGGTCT AGTGAATCTG CACAGAAGGC CCTTAAGATC 600  
 ATGCAACAGA TGAGTGACCA CGCTACGAC AAACCTACTG TGCTGATGA CATAGCAGCA 660  
 AACTGTATAT ATCTAAATAT CCCCACAAA GGGCACGTCT TGCTGCACCG AACCCCGGAA 720  
 GAGTATCCAG AAAGTGCAA GGTATTATGAG AAACCTGAAG ACCATATGCT GATCCCGGTG 780  
 AGCATGTCTG AACTGGAAAA GGTGGATGGG CTGCTCACCT GCTGCTCAGT TTTAATTAAC 840  
 AAGAAGGTAG ACTCCTGA 858

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Gly Leu Gly His Pro Ser Ala Phe Gly Arg Ala Thr His Ala  
 1 5 10 15  
 Val Val Arg Ala Leu Pro Glu Ser Leu Cys Gln His Ala Leu Arg Ser  
 20 25 30  
 Ala Lys Gly Glu Glu Val Asp Val Ala Arg Ala Glu Arg Gln His Gln  
 35 40 45  
 Leu Tyr Val Gly Val Leu Gly Ser Lys Leu Gly Leu Gln Val Val Glu  
 50 55 60  
 Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys Val Phe Val Glu Asp Val  
 65 70 75 80  
 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro  
 85 90 95  
 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu  
 100 105 110  
 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly  
 115 120 125

Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys  
 130 135 140  
 Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu Ala Asp Thr Phe Lys Asp  
 145 150 155 160  
 Tyr Ala Val Ser Thr Val Pro Val Ala Asp Gly Leu His Leu Lys Ser  
 165 170 175  
 Phe Cys Ser Met Ala Gly Pro Asn Leu Ile Ala Ile Gly Ser Ser Glu  
 180 185 190  
 Ser Ala Gln Lys Ala Leu Lys Ile Met Gln Gln Met Ser Asp His Arg  
 195 200 205  
 Tyr Asp Lys Leu Thr Val Pro Asp Asp Ile Ala Ala Asn Cys Ile Tyr  
 210 215 220  
 Leu Asn Ile Pro Asn Lys Gly His Val Leu Leu His Arg Thr Pro Glu  
 225 230 235 240  
 Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu Lys Leu Lys Asp His Met  
 245 250 255  
 Leu Ile Pro Val Ser Met Ser Glu Leu Glu Lys Val Asp Gly Leu Leu  
 260 265 270  
 Thr Cys Cys Ser Val Leu Ile Asn Lys Lys Val Asp Ser  
 275 280 285

## (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 858 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATGGGGACGC CGGGGGAGGG GCTGGGCCGC TGCTCCCATG CCCTGATCCG GGGAGTCCCA	60
GAGAGCCTGG CGTCGGGGGA AGGTGCGGGG GCTGGCCTTC CCCTCTGGA TCTGGCCAAA	120
GCTCAAAGGG AGCACGGGCT GCTGGGAGGT AAAGTGAGGC AACGACTGGG GCTACAGCTG	180
CTAGAACTGC CACCTGAGGA GTCATTGCCG CTGGGACCGC TGCTTGGCGA CACGGCCCTG	240
ATCCAAGGGG ACACGGCCCT AATCACGCGG CCTGAGAGCC CCGCTGTAG GCCAGAGGTC	300

GATGGAGTCC GCAAAGCCCT GCAAGACCTG GGGCTCCGAA TTGTGGAAT AGGAGACGAG	360
AACGCGACGC TGGATGTCAC TGACGTTCTC TTCACCGGCC GGGAGTTTTT CGTAGGCCTC	420
TCCAAATGGA CCAATCACCG AGGAGCTGAG ATCGTGGCGG ACACGTTCCG GGACTTCGCC	480
GTCTCCACTG TGCCAGTCTC GGCTCCCTCC CACCTGCGCG GTCTCTGCGG CATGGGGGGA	540
CCTCGCACTG TTGTGGCAGG CAGCAGCGAC GCTGCCCAAA AGGCTGTCCG GGCAATGGCA	600
GTGCTGACAG ATCACCATA TGCCTCCCTG ACCCTCCAG ATGACGACG TGCTGACTGT	660
CTCTTCTCTG GTCTGGGTT GCGTGGTGTG CCCCCTTTCC TCCTGCACCG TGGAGGTGGG	720
GATCTGCCCA ACAGCCAGGA GGCACTGCAG AAGCTCTCTG ATGTCACCCT GGTACCTGTG	780
TCCTGCTCAG AACTGGAGAA AGCTGGCGCC GGGCTCAGCT CCCTCTGCTT GGTGCTCAGC	840
ACACGCCCCC ACAGCTGA	858

## (2) INFORMATION FOR SEQ ID NO: 4:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: protein

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Gly Thr Pro Gly Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile	
1                  5                  10                  15	
Arg Gly Val Pro Glu Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly	
20                  25                  30	
Leu Pro Ala Leu Asp Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu	
35                  40                  45	
Gly Gly Lys Leu Arg Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro	
50                  55                  60	
Pro Glu Glu Ser Leu Pro Leu Gly Pro Leu Leu Gly Asp Thr Ala Val	
65                  70                  75                  80	
Ile Gln Gly Asp Thr Ala Leu Ile Thr Arg Pro Trp Ser Pro Ala Arg	
85                  90                  95	
Arg Pro Glu Val Asp Gly Val Arg Lys Ala Leu Gln Asp Leu Gly Leu	

100	105	110
Arg Ile Val Glu Ile Gly Asp Glu Asn Ala Thr Leu Asp Gly Thr Asp		
115	120	125
Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys Trp Thr		
130	135	140
Asn His Arg Gly Ala Glu Ile Val Ala Asp Thr Phe Arg Asp Phe Ala		
145	150	155
Val Ser Thr Val Pro Val Ser Gly Pro Ser His Leu Arg Gly Leu Cys		
165	170	175
Gly Met Gly Gly Pro Arg Thr Val Val Ala Gly Ser Ser Asp Ala Ala		
180	185	190
Gln Lys Ala Val Arg Ala Met Ala Val Leu Thr Asp His Pro Tyr Ala		
195	200	205
Ser Leu Thr Leu Pro Asp Asp Ala Ala Ala Asp Cys Leu Phe Leu Arg		
210	215	220
Pro Gly Leu Pro Gly Val Pro Pro Phe Leu Leu His Arg Gly Gly Gly		
225	230	235
Asp Leu Pro Asn Ser Gln Glu Ala Leu Gln Lys Leu Ser Asp Val Thr		
245	250	255
Leu Val Pro Val Ser Cys Ser Glu Leu Glu Lys Ala Gly Ala Gly Leu		
260	265	270
Ser Ser Leu Cys Leu Val Leu Ser Thr Arg Pro His Ser		
275	280	285

## (2) INFORMATION FOR SEQ ID NO: 5:

- (1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 777 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GTGCCCAGCA AGAAGGCCCT GGTCCGCCGC CCCAGCCCCA GGCTCGCGGA AGGACTGGTG 60



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ACACACGTCG AGCGGGAGCA GGTGATCAC GGCCTGGCCC TCGAACAGTG GGACGCCTAC   120
GTCGAGGCCC TCGGAGCACA CGGCTGGGAG ACTCTGGAGG TGGACCGGC CGAGTACTGT   180
CCGACTCGG TCTTCGTCGA GGACGCCGTC GTCGTGTTCC GCAACGTGCG GCTGATCAG   240
CGGCCCGGCG CCGAGTCGCG GCGCGCGGAG ACGGCCGCG TCGAGGAGGC CGTGGCCCGG   300
CTCGGTGCT CCGTGAAC TGTTGTGGAG CCGGECACCC TGGACGGCG CGAGTCTCTG   360
AAGATCGGCG ACACGATCTA CGTGGGACGC GGCGGCCGGA CCAACGCGGC CGGTGTCCAG   420
CAGTTGCGGG CGGCGTTCGA GCGCTGGGC GCCCGGTCG TCGCGTGCC CGTGAGCAAG   480
GTGCTGCATC TGAAGTCGGC GGTACCCGCG CTGCGGACG GGACGCTGAT CGGGCACATC   540
CCGCTGACGG ACGTGCCTC GCTGTTCCCG CGTTTCCTGC CGGTGCCGGA GGAGTCGGGG   600
GCGCACGTGG TGTGCTCGG CCGGAGCAGG CTGCTGATGG CGGCGAGCG GCCCAAGACG   660
CGGAGCTGC TCGCGATCT CGGTACGAG CGGTGCTCG TCGACATCGG GGAGTTCGAG   720
AAGCTGGAGG GCTGTGTGAC GTGCCTCTCG GTCAGGCTGC GCGAGCTGTA CGACTGA   777

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## (2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

Val Pro Ser Lys Lys Ala Leu Val Arg Arg Pro Ser Pro Arg Leu Ala
1           5           10          15

Glu Gly Leu Val Thr His Val Glu Arg Glu Gln Val Asp His Gly Leu
20          25          30

Ala Leu Glu Gln Trp Asp Ala Tyr Val Glu Ala Leu Gly Ala His Gly
35          40          45

Trp Glu Thr Leu Glu Val Asp Pro Ala Glu Tyr Cys Pro Asp Ser Val
50          55          60

Phe Val Glu Asp Ala Val Val Val Phe Arg Asn Val Ala Leu Ile Thr

```

-7-

65                      70                      75                      80  
 Arg Pro Gly Ala Glu Ser Arg Arg Ala Glu Thr Ala Gly Val Glu Glu  
                             85                      90                      95  
 Ala Val Ala Arg Leu Gly Cys Ser Val Asn Trp Val Trp Glu Pro Gly  
                             100                      105                      110  
 Thr Leu Asp Gly Gly Asp Val Leu Lys Ile Gly Asp Thr Ile Tyr Val  
                             115                      120                      125  
 Gly Arg Gly Gly Arg Thr Asn Ala Ala Gly Val Gln Gln Leu Arg Ala  
                             130                      135                      140  
 Ala Phe Glu Pro Leu Gly Ala Arg Val Val Ala Val Pro Val Ser Lys  
                             145                      150                      155                      160  
 Val Leu His Leu Lys Ser Ala Val Thr Ala Leu Pro Asp Gly Thr Val  
                             165                      170                      175  
 Ile Gly His Ile Pro Leu Thr Asp Val Pro Ser Leu Phe Pro Arg Phe  
                             180                      185                      190  
 Leu Pro Val Pro Glu Glu Ser Gly Ala His Val Val Leu Leu Gly Gly  
                             195                      200                      205  
 Ser Arg Leu Leu Met Ala Ala Ser Ala Pro Lys Thr Ala Glu Leu Leu  
                             210                      215                      220  
 Ala Asp Leu Gly His Glu Pro Val Leu Val Asp Ile Gly Glu Phe Glu  
                             225                      230                      235                      240  
 Lys Leu Glu Gly Cys Val Thr Cys Leu Ser Val Arg Leu Arg Glu Leu  
                             245                      250                      255  
 Tyr Asp

## (2) INFORMATION FOR SEQ ID NO: 7:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (11) MOLECULE TYPE: cDNA

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ATGTTCAAGC ACATCATCGC TCGCAGCCCC GCCCGCAGCC TGGTCGACGG CCTGACCTCC 60

```

AGCCACCTCG GCAAGCCGGA CTACGCCAAG GCCCTGAGC AGCACAACGC CTACATCCGC 120
GCCTTGCGAGA CCTGCGACGT GGACATCACC CTGCTGCCGC CGGACGAACG CTTCCCGGAC 180
TCGTTGTTTC TCGAGGACCC GGTGCTCTGC ACCTCGCGCT GCGCCATCAT CACCCGCCCC 240
GGCGCCGAAT CGCGCGCGCG CGAGACCGAG ATCATCGAGG AAACCGTGCA GCGCTTCTAT 300
CCGGGCAAGG TCGAGCGCAT CGAGGCACCC GGCACGCTGG AAGCCGGCGA CATCATGATG 360
GTGCGGACCC ACTTCTACAT CGGCGAATCG GCCCGACCA ACGCCGAGGG CGCCGCGCAG 420
ATGATCGCGA TCCTGGAGAA ACATGGCCTC AGCGGCTCGG TGCTGCGCCT GGAAAAGTTC 480
CTGCACCTGA AGACCGGCTT CGCCTACCTG GAACACAACA ACCTGCTGGC CGCGCGCGAG 540
TTGTCAGCA AGCCGGAGTT CCAGGACTTC AACATCATCG AGATCCCCGA AGAGGATCC 600
TACGCCGCCA ACTGCATCTG GGTCAACGAA AGGTGATCA TGCCCGCCGG CTATCCCGGG 660
ACCCGCGAGA AGATCGCCCG CCTCGGCTAC CGGTGATCG AGGTGGACAC CTCGAATAT 720
CGCAAGATCG ACGGCGGCGT CAGTTGCATG TCGCTGCGCT TCTGA 765

```

## (2) INFORMATION FOR SEQ ID NO: 8:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (x1) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

```

Met Phe Lys His Ile Ile Ala Arg Thr Pro Ala Arg Ser Leu Val Asp
1           5           10          15

Gly Leu Thr Ser Ser His Leu Gly Lys Pro Asp Tyr Ala Lys Ala Leu
20          25          30

Glu Gln His Asn Ala Tyr Ile Arg Ala Leu Gln Thr Cys Asp Val Asp
35          40          45

Ile Thr Leu Leu Pro Pro Asp Glu Arg Phe Pro Asp Ser Val Phe Val
50          55          60

Glu Asp Pro Val Leu Cys Thr Ser Arg Cys Ala Ile Ile Thr Arg Pro
65          70          75          80

```

-9-

Gly Ala Glu Ser Arg Arg Gly Glu Thr Glu Ile Ile Glu Glu Thr Val  
                     85                    90                    95  
 Gln Arg Phe Tyr Pro Gly Lys Val Glu Arg Ile Glu Ala Pro Gly Thr  
                     100                    105                    110  
 Val Glu Ala Gly Asp Ile Met Met Val Gly Asp His Phe Tyr Ile Gly  
                     115                    120                    125  
 Glu Ser Ala Arg Thr Asn Ala Glu Gly Ala Arg Gln Met Ile Ala Ile  
                     130                    135                    140  
 Leu Glu Lys His Gly Leu Ser Gly Ser Val Val Arg Leu Glu Lys Val  
                     145                    150                    155                    160  
 Leu His Leu Lys Thr Gly Leu Ala Tyr Leu Glu His Asn Asn Leu Leu  
                     165                    170                    175  
 Ala Ala Gly Glu Phe Val Ser Lys Pro Glu Phe Gln Asp Phe Asn Ile  
                     180                    185                    190  
 Ile Glu Ile Pro Glu Glu Glu Ser Tyr Ala Ala Asn Cys Ile Trp Val  
                     195                    200                    205  
 Asn Glu Arg Val Ile Met Pro Ala Gly Tyr Pro Arg Thr Arg Glu Lys  
                     210                    215                    220  
 Ile Ala Arg Leu Gly Tyr Arg Val Ile Glu Val Asp Thr Ser Glu Tyr  
                     225                    230                    235                    240  
 Arg Lys Ile Asp Gly Gly Val Ser Cys Met Ser Leu Arg Phe  
                     245                    250

## (2) INFORMATION FOR SEQ ID NO: 9:

## (1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(11) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGG AAAAAACAA ACTTGGCGTC CACTCCGAAG CCGGCAAACT GCGCAAAGTG	60
ATGGTCTGCT CGCCCGGACT CGCCACCAG CGCCTGACCC CGAGCAACTG CGACGAGTTG	120
CTGTTGACG ACCTGATCTG GGTGAACCAG GCCAAGCGCG ACCACTTCGA CTTCGTGACC	180

AAGATGCGCG AGCGCGCAT CGAGTCCTC GAGATGCACA ATCTGCTGAC CGAGACCATC	240
CAGAACCCGG AAGCGCTGAA GTGGATCCTC GATCGCAAGA TCACGCGGA CAGCGTCGGC	300
CTGGGCTGA CCAGCGAGCT GCGTCCTGG CTGGAGAGCC TGGAGCCGCG CAAGCTGGCC	360
GASTACCTGA TCGGCGGCT CGCCGCTGAC GACCTGCCCG CCAGCGAAGG CGCCAACATC	420
CTCAAGATGT ACCGCGAGTA CCTGGGCCAT TCCAGTTCC TGCTGCCGCC GTTGCCGAAC	480
ACCCAGTTCA CCGCGACAC CACTTGCTGG ATCTACGGCG GCGTGACCCT GAACCCGATG	540
TACTGGCCGG CGGACGACA GSAACCTG CTGACCAGCG CCATCTACAA GTTCCACCCC	600
GASTTGCCA ACGCCGATT CGAGATCTGG TACGGCGACC CGACAAGGA CCACGGCTCC	660
TCGACCTGG AAGCGCGGA CGTGATGCCG ATCGGCAACG GCGTGTCTCT GATCGGCATG	720
GGCGAGCGCT CCTCGGCCA GGCCATCGGT CAGGTGCGCC AGTGGTGTGTT CGCCAAGGGC	780
GCCGCGAGC GGGTGATCGT CGCCGGCCTG CCGAAGTCC GCGCGCGAT GCACCTGGAC	840
ACCGTGTTC GCTTCTGGA CCGCGACCTG GTCACGCTCT TCCCGAAGT GGTCAAGGAA	900
ATCGTGCCCT TCAGCTGCG CCCGATCGG AGCAGCCCTT ACGCATGAA CATCGCCCGC	960
GAGGAGAAA CCTTCTCGA AGTGGTCGCC GAATCCCTCG GCTGAAGAA ACTGCGCGTG	1020
GTGAGACCG GCGCAACAG CTTGCGCGC GAGCGGAGC AATGGGACGA CGTAACAAC	1080
GTGGTCTGCC TGGAGCGGG CGTGGTGGTC GGCTACGACC GCAACACCTA CACCAACACC	1140
CTGCTGCGCA AGGCCGGCT CGAGGTCATC ACCATCAGCG CCAGCGAACT GGGTCGCGGT	1200
CGCGGGGGG GCCACTGCAT GACCTGCCCG ATCGTCCGCG ACCGATCGA CTACTGA	1257

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Ser	Thr	Glu	Lys	Thr	Lys	Leu	Gly	Val	His	Ser	Glu	Ala	Gly	Lys
1					5				10					15	

Leu Arg Lys Val Met Val Cys Ser Pro Gly Leu Ala His Gln Arg Leu  
 20 25 30  
 Thr Pro Ser Asn Cys Asp Glu Leu Leu Phe Asp Asp Val Ile Trp Val  
 35 40 45  
 Asn Gln Ala Lys Arg Asp His Phe Asp Phe Val Thr Lys Met Arg Glu  
 50 55 60  
 Arg Gly Ile Asp Val Leu Glu Met His Asn Leu Leu Thr Glu Thr Ile  
 65 70 75 80  
 Gln Asn Pro Glu Ala Leu Lys Trp Ile Leu Asp Arg Lys Ile Thr Ala  
 85 90 95  
 Asp Ser Val Gly Leu Gly Leu Thr Ser Glu Leu Arg Ser Trp Leu Glu  
 100 105 110  
 Ser Leu Glu Pro Arg Lys Leu Ala Glu Tyr Leu Ile Gly Gly Val Ala  
 115 120 125  
 Ala Asp Asp Leu Pro Ala Ser Glu Gly Ala Asn Ile Leu Lys Met Tyr  
 130 135 140  
 Arg Glu Tyr Leu Gly His Ser Ser Phe Leu Leu Pro Pro Leu Pro Asn  
 145 150 155 160  
 Thr Gln Phe Thr Arg Asp Thr Thr Cys Trp Ile Tyr Gly Gly Val Thr  
 165 170 175  
 Leu Asn Pro Met Tyr Trp Pro Ala Arg Arg Gln Glu Thr Leu Leu Thr  
 180 185 190  
 Thr Ala Ile Tyr Lys Phe His Pro Glu Phe Ala Asn Ala Glu Phe Glu  
 195 200 205  
 Ile Trp Tyr Gly Asp Pro Asp Lys Asp His Gly Ser Ser Thr Leu Glu  
 210 215 220  
 Gly Gly Asp Val Met Pro Ile Gly Asn Gly Val Val Leu Ile Gly Met  
 225 230 235 240  
 Gly Glu Arg Ser Ser Arg Gln Ala Ile Gly Gln Val Ala Gln Ser Leu  
 245 250 255  
 Phe Ala Lys Gly Ala Ala Glu Arg Val Ile Val Ala Gly Leu Pro Lys  
 260 265 270  
 Ser Arg Ala Ala Met His Leu Asp Thr Val Phe Ser Phe Cys Asp Arg  
 275 280 285

Asp Leu Val Thr Val Phe Pro Glu Val Val Lys Glu Ile Val Pro Phe  
290 295 300

Ser Leu Arg Pro Asp Pro Ser Ser Pro Tyr Gly Met Asn Ile Arg Arg  
305 310 315 320

Glu Glu Lys Thr Phe Leu Glu Val Val Ala Glu Ser Leu Gly Leu Lys  
325 330 335

Lys Leu Arg Val Val Glu Thr Gly Gly Asn Ser Phe Ala Ala Glu Arg  
340 345 350

Glu Gln Trp Asp Asp Gly Asn Asn Val Val Cys Leu Glu Pro Gly Val  
355 360 365

Val Val Gly Tyr Asp Arg Asn Thr Tyr Thr Asn Thr Leu Leu Arg Lys  
370 375 380

Ala Gly Val Glu Val Ile Thr Ile Ser Ala Ser Glu Leu Gly Arg Gly  
385 390 395 400

Arg Gly Gly Gly His Cys Met Thr Cys Pro Ile Val Arg Asp Pro Ile  
405 410 415

Asp Tyr

(2) INFORMATION FOR SEQ ID NO: 11:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1014 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGTATCAAT GGAAATACG CAACGACCAT CGTTTGATTG TGAAATCAGA GCCAAATATC	60
GTTGGTTTAT GACGGATTCC TACGTCBCTG CTGCCCGTCT AGGGTCACCT GCACGCCGCA	120
CCCCCGGAC GCGGCGSTAT GCAATGACCC CGCCGGCCTT CTTTGGCGTC GCATACGCGA	180
TCAACCCCTG GATGGACGTC ACCGCGCCAG TCGACGTCCA AGTCGCGCAA GCACAGTGGG	240
AGCACCTCCA CCAGACCTAT CTTCGGCTAG GCCACAGCGT GGATCTGATC GAGCCCATTT	300
CCGGGTTACC GGACATGGTG TACACCGCCA ACGGTGGGTT CATCGCGCAC GACATCGCGG	360

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TGGTCGCCCG GTTCGGTTC CCGAACGAG CTGGTGAGTC TAGAGCCTAT GCCAGCTGGA 420
TGTCTCGGT CCGATATCGC CCGGTGACCA CCGCCACGT CAACGAGGA CAGGGCGACC 480
TGCTGATGT TGGGAAAGG GTGTTGGCGG GCTACGGCTT TCGACAGAC CAGCGCGAC 540
ACGCCGAAAT CGCCGCGTG CTGGTCTGC CCGTGTCTC CCTCGAGTTG GTCGACCCAC 600
GGTTCTATCA CCGGACACC GCGTGGCCG TCTCGACGA CCACAGATC GCTACTACC 660
CGCCGCGGT CAGTACGCA GCGCAGAAC AGTTGTGGC GCTGTCCCG GACGCGATTG 720
TGGTCGCGAG TGGGACGCG TTCGTGTCG GACTCAACG CGTCTGAC GGTCTGAACG 780
TAGTGCTTC GGTGCGGCC ATGGGTTTG CCGCGCAAT ACGCGAGCC GGCTTCGAGC 840
CGGTCGGTG CGATCTGCC GAGTGTCTA AGGCGGCGG TTCCGTCAAG TGCTGCACGC 900
TGGAGATACA CCCATGACAA ATCTCGCGA TGCCACTCAG GCCACTATGG CACTGGTCGA 960
AAGGCATGCA GCGACAATT ATCGCCGCT GCCTGTGGTG GCGGCCAGCG CTGA 1014

```

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

Asn Val Ser Met Glu Asn Thr Gln Arg Pro Ser Phe Asp Cys Glu Ile
1           5           10           15
Arg Ala Lys Tyr Arg Trp Phe Met Thr Asp Ser Tyr Val Ala Ala Ala
20          25          30
Arg Leu Gly Ser Pro Ala Arg Arg Thr Pro Arg Thr Arg Arg Tyr Ala
35          40          45
Met Thr Pro Pro Ala Phe Phe Ala Val Ala Tyr Ala Ile Asn Pro Trp
50          55          60
Met Asp Val Thr Ala Pro Val Asp Val Gln Val Ala Gln Ala Gln Trp
65          70          75          80
Glu His Leu His Gln Thr Tyr Leu Arg Leu Gly His Ser Val Asp Leu
85          90          95

```



Ile Glu Pro Ile Ser Gly Leu Pro Asp Met Val Tyr Thr Ala Asn Gly  
100 105 110

Gly Phe Ile Ala His Asp Ile Ala Val Val Ala Arg Phe Arg Phe Pro  
115 120 125

Glu Arg Ala Gly Glu Ser Arg Ala Tyr Ala Ser Trp Met Ser Ser Val  
130 135 140

Gly Tyr Arg Pro Val Thr Thr Arg His Val Asn Glu Gly Gln Gly Asp  
145 150 155 160

Leu Leu Met Val Gly Glu Arg Val Leu Ala Gly Tyr Gly Phe Arg Thr  
165 170 175

Asp Gln Arg Ala His Ala Glu Ile Ala Ala Val Leu Gly Leu Pro Val  
180 185 190

Val Ser Leu Glu Leu Val Asp Pro Arg Phe Tyr His Leu Asp Thr Ala  
195 200 205

Leu Ala Val Leu Asp Asp His Thr Ile Ala Tyr Tyr Pro Pro Ala Phe  
210 215 220

Ser Thr Ala Ala Gln Glu Gln Leu Ser Ala Leu Phe Pro Asp Ala Ile  
225 230 235 240

Val Val Gly Ser Ala Asp Ala Phe Val Phe Gly Leu Asn Ala Val Ser  
245 250 255

Asp Gly Leu Asn Val Val Leu Pro Val Ala Ala Met Gly Phe Ala Ala  
260 265 270

Gln Leu Arg Ala Ala Gly Phe Glu Pro Val Gly Val Asp Leu Ser Glu  
275 280 285

Leu Leu Lys Gly Gly Gly Ser Val Lys Cys Cys Thr Leu Glu Ile His  
290 295 300

Pro  
305